

**Blast 2 Sequences results**

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Entrez

BLAST

OMIM

Taxonomy

Structure

**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]**

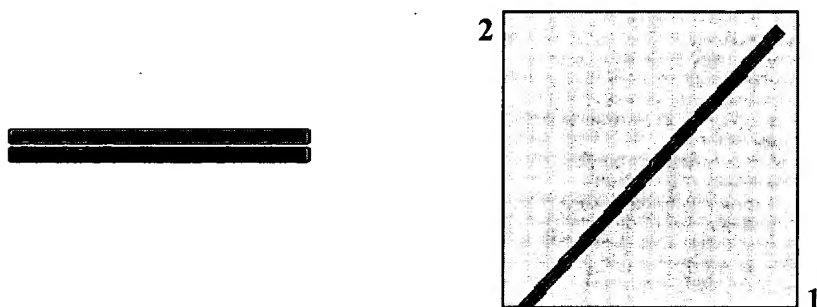
Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ View option **Standard**  
Masking character option **X for protein, n for nucleotide** Masking color option **Black**  
☐ Show CDS translation **Align**

**Sequence 1:** lcl|seq\_1

Length = 14 (1 .. 14)

**Sequence 2:** lcl|seq\_2

Length = 14 (1 .. 14)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 34.3 bits (77), Expect = 0.76  
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 0/14 (0%)

Query 1 AGCKNFFWKTFTSC 14  
AGCKNF+WK FTSC  
Sbjct 1 AGCKNFYWKGFTSC 14

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda K H  
0.334 0.138 0.589

Gapped  
Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Sequences: 1  
Number of Hits to DB: 16  
Number of extensions: 5  
Number of successful extensions: 1  
Number of sequences better than 10.0: 1  
Number of HSP's gapped: 1  
Number of HSP's successfully gapped: 1  
Length of query: 14  
Length of database: 1,129,354,045  
Length adjustment: 0  
Effective length of query: 14  
Effective length of database: 1,129,354,045  
Effective search space: 15810956630  
Effective search space used: 15810956630  
Neighboring words threshold: 9  
X1: 15 ( 7.2 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 39 (21.7 bits)  
S2: 68 (30.8 bits)